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DATE: Wednesday, February 21, 2007

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☐	L5	(increas$ or enhanc$ or improv$) near3 L4	460
☐	L4	sequence near3 L1	5434
☐	L3	sequence same L2	1201
☐	L2	(increas$ or enhanc$ or improv$) near3 L1	2495
☐	L1	translat$ near3 efficien$	18253

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         to 50,000
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 NEWS 25 JAN 29  CAS Registry Number crossover limit increased to 300,000 in
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=> s translat? (3a) efficien?
L1       9086 TRANSLAT? (3A) EFFICIEN?

=> s l1 and sequence
L2       3237 L1 AND SEQUENCE

=> s (improv? or increas? or enhanc? or regulat?) and l2
L3       1970 (IMPROV? OR INCREAS? OR ENHANC? OR REGULAT?) AND L2

=> s l3 and polyribosom?
L4         20 L3 AND POLYRIBOSOM?

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L5         12 DUP REM L4 (8 DUPLICATES REMOVED)

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L5  ANSWER 1 OF 12  CAPLUS  COPYRIGHT 2007 ACS on STN
AN  2006:117096  CAPLUS <<LOGINID::20070222>>
DN  144:186045
TI  Nucleic acid sequences having translation  ***enhancement***  activity
    and use
IN  Sawasaki, Tatsuya; Endo, Yaeta; Kamura, Nami
PA  Cellfree Sciences Co., Ltd., Japan
SO  U.S. Pat. Appl. Publ., 16 pp.
    CODEN: USXXCO
DT  Patent
LA  English
FAN.CNT 1
    PATENT NO.         KIND  DATE       APPLICATION NO.      DATE
    ---------------    ----  --------   -------------------  --------
PI  US 2006029999      A1    20060209   US 2005-53594        20050208
    JP 2006042676      A     20060216   JP 2004-227866       20040804
PRAI JP 2004-227866    A     20040804
AB  The present invention provides a polynucleotide comprising a nucleic acid
    ***sequence***  having an activity of  ***regulating***  the
    ***translation***  ***efficiency***  of a template in a cell-free
    protein synthesis system and also provides a method for utilizing the
    same, etc. Protein synthesis is carried out by a translation template
    contg. a polynucleotide comprising a nucleic acid  ***sequence***  which
    is to be an object to be selected, a  ***polyribosome***  fraction is
    prepd. from the reaction soln. and a nucleic acid  ***sequence***
    bonding to ribosome is analyzed whereupon a selection is done.

L5  ANSWER 2 OF 12  EMBASE  COPYRIGHT (c) 2007 Elsevier B.V. All rights
    reserved on STN
AN  2006272492  EMBASE  <<LOGINID::20070222>>
TI  RNA helicase A is necessary for translation of selected messenger RNAs.
AU  Hartman T.R.; Qian S.; Bolinger C.; Fernandez S.; Schoenberg D.R.;
    Boris-Lawrie K.
CS  K. Boris-Lawrie, Center for Retrovirus Research, Department of Veterinary
    Biosciences, Ohio State University, Columbus, OH 43210, United States.
    boris-lawrie.1@osu.edu
SO  Nature Structural and Molecular Biology, (26 Jun 2006) Vol. 13, No. 6, pp.
    509-516. .
    Refs: 50
    ISSN: 1545-9993  E-ISSN: 1545-9985  CODEN: NSMBCU
PUI N1092
CY  United States
DT  Journal; Article
FS  022  Human Genetics
    029  Clinical Biochemistry
LA  English
SL  English
ED  Entered STN: 4 Aug 2006
    Last Updated on STN: 4 Aug 2006
AB  RNA helicase A (RHA) is a highly conserved DEAD-box protein that activates
    transcription, modulates RNA splicing and binds the nuclear pore complex.
    The life cycle of typical mRNA involves RNA processing and translation
    after ribosome scanning of a relatively unstructured 5' untranslated
    region (UTR). The precursor RNAs of retroviruses and selected cellular
    genes harbor a complex 5' UTR and use a yet-to-be-identified host
    post-transcriptional effector to stimulate  ***efficient***
    ***translation*** . Here we show that RHA recognizes a structured
    5'-terminal post-transcriptional control element (PCE) of a retrovirus and
    the JUND growth-control gene. RHA interacts with PCE RNA in the nucleus
    and cytoplasm, facilitates  ***polyribosome***  association and is
    necessary for its  ***efficient***  ***translation*** . Our results
    reveal a previously unidentified role for RHA in translation and implicate
    RHA as an integrative effector in the continuum of gene expression from
    transcription to translation. .COPYRGT. 2006 Nature Publishing Group.

L5  ANSWER 3 OF 12  EMBASE  COPYRIGHT (c) 2007 Elsevier B.V. All rights
    reserved on STN
AN  2006260551  EMBASE  <<LOGINID::20070222>>
TI  In vitro selection of translational  ***regulatory***  elements.
```

AU Nagao I.; Obokata J.
CS J. Obokata, Center for Gene Research, Nagoya University, Nagoya, 464-8602,
Japan. obokata@gene.nagoya-u.ac.jp
SO Analytical Biochemistry, (1 Jul 2006) Vol. 354, No. 1, pp. 1-7. .
Refs: 38
ISSN: 0003-2697 E-ISSN: 1096-0309 CODEN: ANBCA2
PUI S 0003-2697(06)00243-0
CY United States
DT Journal; Article
FS 029 Clinical Biochemistry
LA English
SL English
ED Entered STN: 4 Jul 2006
Last Updated on STN: 4 Jul 2006
AB Untranslated regions (UTRs) of mRNAs carry various kinds of translational ***regulatory*** elements; however, our knowledge of them is still limited. We created an in vitro selection system that allows us to make a systematic enrichment of the sequences that alter ***translation*** ***efficiency*** (SESTRE) in any given mRNA and translation system. This method consists of the introduction of random nucleotide sequences into the UTRs of given mRNAs, followed by translation, size fractionation of the ***polyribosomes*** , and reverse transcription and PCR amplification (RT-PCR), with repeated cycles of these steps to enrich highly or poorly translatable mRNAs. With this experimental method, we examined how and where translational ***enhancer*** motifs emerge on mRNAs using the in vitro translation systems of wheat germ extract. The results indicate that the translational ***enhancers*** differentially emerge in response to the presence or absence of the 5' cap. Interestingly, the translational ***enhancers*** that activate cap-independent translation evolved more readily in the 3' UTR than in the 5' UTR in wheat germ extract. This SESTRE method should be a powerful tool with which to ***improve*** the ***translational*** ***efficiency*** of given mRNAs in given translation systems and to investigate the structure-function relationship of eukaryotic mRNAs underlying translational control. .COPYRGT. 2006 Elsevier Inc. All rights reserved.

L5 ANSWER 4 OF 12 EMBASE COPYRIGHT (c) 2007 Elsevier B.V. All rights reserved on STN DUPLICATE 1
AN 2004168536 EMBASE <<LOGINID::20070222>>
TI Inhibition of Glutamate Receptor 2 Translation by a Polymorphic Repeat ***Sequence*** in the 5'-Untranslated Leaders.
AU Myers S.J.; Huang Y.; Genetta T.; Dingledine R.
CS R. Dingledine, Department of Pharmacology, Emory University School of Medicine, Atlanta, GA 30322, United States. rdingledine@pharm.emory.edu
SO Journal of Neuroscience, (7 Apr 2004) Vol. 24, No. 14, pp. 3489-3499. .
Refs: 56
ISSN: 0270-6474 CODEN: JNRSDS
CY United States
DT Journal; Article
FS 002 Physiology
008 Neurology and Neurosurgery
029 Clinical Biochemistry
LA English
SL English
ED Entered STN: 13 May 2004
Last Updated on STN: 13 May 2004
AB Previous studies have identified multiple transcription initiation sites for the glutamate receptor 2 (GluR2) gene, resulting in a heterogeneous population of GluR2 transcripts in vivo that differ in the length of their 5'-untranslated leaders (5'-UTR). We designed a series of monocistronic and dicistronic GluR2 cDNA constructs that model the natural in vivo transcripts and investigated their ***translation*** ***efficiencies*** in rabbit reticulocyte lysates, Xenopus oocytes, and primary cultured neurons. Transcripts containing long 5' leaders (429 and 481 bases) were translated poorly compared with those with shorter leaders (341 or fewer bases). None of the five initiation codons in the 5'-UTR or the leader length per se were responsible for translation ***regulation*** . Rather, control of translation was mediated by a ***sequence*** containing a 34-42 nucleotide imperfect GU repeat predicted to form secondary structure in vivo. This translation suppression domain is included in some but not all rat and human GluR2 transcripts in vivo, depending on the site of transcription initiation. Rat cortex GluR2 transcripts that lack the translation suppression ***sequence*** were preferentially associated with ***polyribosomes*** . Furthermore, the GU-repeat cluster was found to be polymorphic in humans, raising the possibility that expansion or contraction of the GU-repeat cluster in certain populations might modify the level of GluR2 protein expression in neurons.

L5 ANSWER 5 OF 12 CAPLUS COPYRIGHT 2007 ACS on STN
AN 2003:532764 CAPLUS <<LOGINID::20070222>>
DN 139:80165
TI Isolating nucleotide ***sequence*** ***regulating*** the ***translation*** ***efficiency*** in cell-free protein synthesis system
IN Endo, Yaeta; Sawasaki, Tatsuya
PA Japan
SO PCT Int. Appl., 89 pp.
CODEN: PIXXD2
DT Patent
LA Japanese

FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2003056009	A1	20030710	WO 2002-JP13756	20021227
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
CA 2471667	A1	20030710	CA 2002-2471667	20021227
AU 2002367144	A1	20030715	AU 2002-367144	20021227
EP 1466972	A1	20041013	EP 2002-790919	20021227
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, SK				
JP 3701292	B2	20050928	JP 2003-556526	20021227
US 2004248140	A1	20041209	US 2004-500346	20040729
PRAI JP 2001-396941	A	20011227		
WO 2002-JP13756	W	20021227		

AB A method of prepg. a polynucleotide contg. a nucleotide ***sequence*** which ***regulate*** the ***translation*** ***efficiency*** of a template in a protein synthesis system, comprising (a) applying a template contg. one or more arbitrary nucleotide sequences to a protein synthesis reaction system, (b) after reacting, recovering a ***polyribosome*** fraction from the liq. reaction mixt., and (c) collecting a polynucleotide contg. the nucleotide ***sequence*** in the template from the ***polyribosome*** fraction; novel polynucleotides ***regulating*** the ***translation*** ***efficiency*** obtained by the above method; a method of synthesizing a protein with the use of a template contg. such a polynucleotide; and so on. Use of d. gradient centrifugation for collecting ***polyribosome*** fraction is claimed. Isolation of 27 57nt randomized sequences and 96 22nt randomized sequences are reported.
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 6 OF 12 BIOSIS COPYRIGHT (c) 2007 The Thomson Corporation on STN
AN 2004:194748 BIOSIS <<LOGINID::20070222>>
DN PREV200400195307
TI Alteration of subcellular distribution of tyrosine hydroxylase (TH) mRNA in rat adrenal medulla and PC12 cells.
AU Xu, L. [Reprint Author]; Baoyong, S. [Reprint Author]; Tank, A. W. [Reprint Author]
CS Dept. of Pharmacol. and Physiology, Univ. of Rochester Med. Ctr., Rochester, NY, USA
SO Society for Neuroscience Abstract Viewer and Itinerary Planner, (2003) Vol. 2003, pp. Abstract No. 157.3. http://sfn.scholarone.com. e-file. Meeting Info.: 33rd Annual Meeting of the Society of Neuroscience. New Orleans, LA, USA. November 08-12, 2003. Society of Neuroscience.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 14 Apr 2004
Last Updated on STN: 14 Apr 2004
AB Posttranscriptional mechanisms have been shown to be important in the ***regulation*** of tyrosine hydroxylase (TH) gene expression. In previous studies, we found that the muscarinic acetylcholine receptor agonist, bethanechol, induced TH mRNA but not TH protein in rat adrenal medulla. In contrast nicotine induced both TH mRNA and TH protein in rat adrenal medulla. Similarly it has been reported that a single immobilization leads to a large induction in adrenal TH mRNA but a very small induction in TH protein. In PC12 cells we have observed that treatment with phorbol ester or high K+ leads to induction of TH mRNA without concomitant ***increase*** in TH protein. These observations suggest that TH gene expression is ***regulated*** at the translational level. In this study, we provide evidence for the possibility that TH mRNA ***translational*** ***efficiency*** is changed due to alterations in the subcellular distribution of TH mRNA in rat adrenal medulla and PC12 cells. Subcellular fractions containing mRNP, monoribosomes and ***polyribosomes*** were separated using linear sucrose gradients. TH mRNA distribution in these fractions was determined using a semi-quantitative RT-PCR assay. We found that TH mRNA was localized mainly in ***polyribosomal*** and monoribosomal fractions and that the distribution of TH mRNA between these fractions was shifted by different stimuli. Our data are consistent with the hypothesis that the ***translational*** ***efficiency*** of TH mRNA is ***regulated*** via differential subcellular distribution in response to activation of different signaling pathways. The detailed mechanisms including TH mRNA ***sequence*** and trans-acting factors responsible for this translational ***regulation*** are under investigation.

L5 ANSWER 7 OF 12 EMBASE COPYRIGHT (c) 2007 Elsevier B.V. All rights reserved on STN
AN 2002141977 EMBASE <<LOGINID::20070222>>
TI Replacement of the yeast TRP4 3' untranslated region by a hammerhead ribozyme results in a stable and efficiently exported mRNA that lacks a poly(A) tail.

AU Duvel K.; Valerius O.; Mangus D.A.; Jacobson A.; Braus G.H.
CS G.H. Braus, Inst. of Microbiology and Genetics, Georg-August-University, Grisebachstr. 8, D-37077 Gottingen, Germany. gbraus@gwdg.de
SO RNA, (2002) Vol. 8, No. 3, pp. 336-344. .
Refs: 51
ISSN: 1355-8382 CODEN: RNARFU
CY United States
DT Journal; Article
FS 004 Microbiology
LA English
SL English
ED Entered STN: 2 May 2002
Last Updated on STN: 2 May 2002
AB The mRNA poly(A) tail serves different purposes, including the facilitation of nuclear export, mRNA stabilization, ***efficient*** ***translation*** , and, finally, specific degradation. The posttranscriptional addition of a poly(A) tail depends on ***sequence*** motifs in the 3' untranslated region (3' UTR) of the mRNA and a complex trans-acting protein machinery. In this study, we have replaced the 3' UTR of the yeast TRP4 gene with sequences encoding a hammerhead ribozyme
that efficiently cleaves itself in vivo. Expression of the TRP4-ribozyme allele resulted in the accumulation of a nonpolyadenylated mRNA. Cells expressing the TRP4-ribozyme mRNA showed a reduced growth rate due to a reduction in Trp4p enzyme activity. The reduction in enzyme activity was not caused by inefficient mRNA export from the nucleus or mRNA destabilization. Rather, analyses of mRNA association with ***polyribosomes*** indicate that translation of the ribozyme-containing mRNA is impaired. This translational defect allows sufficient synthesis of Trp4p to support growth of trp4 cells, but is, nevertheless, of such magnitude as to activate the general control network of amino acid biosynthesis.

L5 ANSWER 8 OF 12 EMBASE COPYRIGHT (c) 2007 Elsevier B.V. All rights reserved on STN
AN 2000136717 EMBASE <<LOGINID::20070222>>
TI Post-transcriptional ***regulation*** of rat CYP2E1 expression: Role of CYP2E1 mRNA untranslated regions in control of ***translational*** ***efficiency*** and message stability.
AU Kocarek T.A.; Zangar R.C.; Novak R.F.
CS R.F. Novak, Institute of Chemical Toxicology, Wayne State University, 2727 Second Avenue, Detroit, MI 48201, United States. r.novak@wayne.edu
SO Archives of Biochemistry and Biophysics, (1 Apr 2000) Vol. 376, No. 1, pp. 180-190. .
Refs: 27
ISSN: 0003-9861 CODEN: ABBIA4
CY United States
DT Journal; Article
FS 022 Human Genetics
029 Clinical Biochemistry
LA English
SL English
ED Entered STN: 4 May 2000
Last Updated on STN: 4 May 2000
AB Altered expression of hepatic CYP2E1 by xenobiotic or physiological stimuli is largely mediated through post-transcriptional mechanisms that may include altered CYP2E1 mRNA translation and/or protein degradation. Examination of the ***polyribosomal*** distribution of rat hepatic P450 mRNAs indicated that, whereas nearly all of the CYP2B, CYP3A, and CYP4A mRNAs were recovered in the polysomal fractions, indicating active translation, approximately 30-40% of CYP2E1 mRNA was not associated with polysomes and therefore not actively engaged in protein synthesis. To examine the CYP2E1 mRNA molecule for sequences that might affect its ***translational*** ***efficiency*** , a series of CYP2E1 recombinant RNAs (rcRNAs) with modified 5' or 3' untranslated regions (UTRs) was translated in vitro using the rabbit reticulocyte lysate system. Deletion of most of the CYP2E1 5' UTR, which was predicted to contain secondary structure, ***increased*** in vitro CYP2E1 protein synthesis. Polysomal distribution analyses of 5'-modified rcRNAs demonstrated that, as seen for hepatic CYP2E1 mRNA, a substantial fraction of each CYP2E1 rcRNA was not associated with polysomes. The polysomal distribution analyses of the CYP2E1 rcRNAs also confirmed that the observed changes in CYP2E1 protein synthesis were associated with altered ribosomal loading. Deletion of the poly(A) tail, and partial or complete deletion of the 3' UTR, decreased CYP2E1 protein synthesis. These changes in protein synthesis were accompanied by ***increased*** degradation of the CYP2E1 rcRNAs. Incubation with translational inhibitors, but not ***increased*** levels of RNase inhibitor, decreased the degradation of the rcRNAs during in vitro translation. In conclusion, these studies suggest that secondary structure in the 5' UTR of CYP2E1 mRNA is at least partially responsible for the inefficient translation of this mRNA. The poly(A) tail and sequences contained within the 3' UTR appear to be important for protecting CYP2E1 mRNA from RNase activity associated with the translation machinery. (C) 2000 Academic Press.

L5 ANSWER 9 OF 12 EMBASE COPYRIGHT (c) 2007 Elsevier B.V. All rights reserved on STN DUPLICATE 2
AN 96153939 EMBASE <<LOGINID::20070222>>
DN 1996153939
TI ***Regulation*** of gene expression for translation initiation factor eIF-2.alpha.: Importance of the 3' untranslated region.
AU Miyamoto S.; Chiorini J.A.; Urcelay E.; Safer B.
CS Molecular Hematology Branch, Section Protein and RNA Biosynthesis, NHLBI, 10 Center Dr MSC 1654,Bethesda, MD 20892-1654, United States
SO Biochemical Journal, (1996) Vol. 315, No. 3, pp. 791-798. .
ISSN: 0264-6021 CODEN: BIJOAK
CY United Kingdom
DT Journal; Article
FS 022 Human Genetics
029 Clinical Biochemistry
LA English
SL English
ED Entered STN: 4 Jun 1996
Last Updated on STN: 4 Jun 1996
AB Gene expression of the a-subunit of eukaryotic initiation factor-2 (eIF-2.alpha.), involves transcriptional and post-transcriptional mechanisms. eIF-2.alpha. is a single-copy gene expressing two mRNAs, 1.6 and 4.2 kb in size. Cloning and sequencing of the cDNA for the 4.2 kb mRNA revealed that it is the result of alternative polyadenylation site selection. Four polyadenylation sites were identified within the 3' untranslated region (UTR) of eIF-2.alpha., only two of which are normally utilized in human and mouse tissues. A functional role for the extended 3' UTR was assessed by comparing the translatability and stability of the 1.6 and kb mRNAs. Both the 1.6 and 4.2 kb transcripts could be translated in vitro and were identified in vivo as being distributed on large ***polyribosomes*** . This indicates that both mRNAs are ***efficiently*** ***translated*** . Stability studies showed that in activated T-cells the 4.2 kb mRNA was more stable than the 1.6 kb mRNA. Polyadenylation site selection and mRNA stability differ for the two mRNAs of eIF-2.alpha.. These activities might be modulated by ***sequence*** elements contained within the untranslated regions of the eIF-2.alpha. gene.

L5 ANSWER 10 OF 12 EMBASE COPYRIGHT (c) 2007 Elsevier B.V. All rights reserved on STN
AN 92134180 EMBASE <<LOGINID::20070222>>
DN 1992134180
TI The iron ***regulatory*** region of ferritin mRNA is also a positive control element for iron-independent translation.
AU Dix D.J.; Lin P.-N.; Kimata Y.; Theil E.C.
CS Department of Biochemistry, North Carolina State University,Raleigh, NC 27695-7622, United States
SO Biochemistry, (1992) Vol. 31, No. 10, pp. 2818-2822. .
ISSN: 0006-2960 CODEN: BICHAW
CY United States
DT Journal; Article
FS 022 Human Genetics
LA English
SL English
ED Entered STN: 24 May 1992
Last Updated on STN: 24 May 1992
AB The iron ***regulatory*** element (IRE) in the 5'-untranslated region of ferritin mRNA interacts with a specific ***regulator*** protein (P-90, IRE-BP, or FRP) to block translation. High cellular iron changes the IRE/P-90 interaction to relax the translational block and allow ***polyribosome*** formation. We now show that the IRE and base-paired flanking regions also ***enhance*** translation in the absence of P-90, explaining the high ***translational*** ***efficiency*** of deregulated ferritin mRNA observed previously. The effect of the IRE on ***translational*** ***efficiency*** was examined by comparing four sets of mRNAs: (1) .+-.IRE in animal (frog) ferritin, ***regulated*** translationally by iron in vivo; (2) .+-.animal IRE fused with plant (soybean) ferritin, ***regulated*** transcriptionally by iron in vivo; (3) repositioned IRE in animal ferritin; (4) mutated IRE in animal ferritin with G16A substitution, which decreases P- 90 binding (negative control). The IRE region ***increased*** ***translational*** ***efficiency*** of both the animal ferritin and the heterologous IRE/soybean ferritin fusion mRNAs; the effect was observed in cell-free translation systems from either plants (wheat germ) or animals (rabbit reticulocyte). Repositioning the IRE further from the 5' cap eliminated positive control of translation. The single base mutation had no effect, indicating that positive and negative translational control involves different sections of the IRE region. Thus, the IRE region in ferritin mRNA encodes both positive translational control and, when combined with the ***regulator*** protein P-90, negative translational control.

L5 ANSWER 11 OF 12 EMBASE COPYRIGHT (c) 2007 Elsevier B.V. All rights reserved on STN DUPLICATE 3
AN 90349590 EMBASE <<LOGINID::20070222>>
DN 1990349590
TI Translation of the Saccharomyces cerevisiae tcm1 gene in the absence of a 5'-untranslated leader.
AU Maicas E.; Shago M.; Friesen J.D.
CS Hospital for Sick Children, 555 University Avenue, Toronto, Ont., Canada
SO Nucleic Acids Research, (1990) Vol. 18, No. 19, pp. 5823-5828. .
ISSN: 0305-1048 CODEN: NARHAD
CY United Kingdom
DT Journal; Article
FS 004 Microbiology
LA English
SL English
ED Entered STN: 13 Dec 1991
Last Updated on STN: 13 Dec 1991
AB The role of eukaryotic 5'-untranslated messenger RNA leaders is not entirely clear, since they share little ***sequence*** similarity among each other. The importance of the leader in determining the

efficiency of ***translation*** initiation was addressed here by examining the ***polyribosome*** distribution of several leader-deletion alleles of the yeast tcm1 gene (coding for ribosomal protein L3). Shortening of this 22-nucleotide leader, or complete removal of it (the first nucleotide of the mRNA becoming the A of the translation initiation codon AUG) permitted translation, albeit reduced. Further deletion of as few as the first two nucleotides of the initiation codon leads to a substantial reduction in ribosome loading, which is compatible with inefficient initiation at the next downstream, out-of-frame, AUG triplet. A second measure of translation initiation was obtained by assaying qualitatively for the production of biologically active L3 protein using growth-resistance to trichodermin. This experiment indicates that ribosomes can recognize the correct initiation codon even in the complete absence of a leader. We conclude that the 5'-untranslated leader of the yeast tcm1 gene is not essential for accurate translation initiation, but ***enhances*** its efficiency.

L5 ANSWER 12 OF 12 EMBASE COPYRIGHT (c) 2007 Elsevier B.V. All rights reserved on STN DUPLICATE 4
AN 89210656 EMBASE <<LOGINID::20070222>>
DN 1989210656
TI Cap-independent translation of mRNA conferred by encephalomyocarditis virus 5' ***sequence*** ***improves*** the performance of the vaccinia virus/bacteriophage T7 hybrid expression system.
AU Elroy-Stein O.; Fuerst T.R.; Moss B.
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AB A recombinant vaccinia virus that directs the synthesis of bacteriophage T7 RNA polymerase provides the basis for the expression of genes that are ***regulated*** by T7 promoters in mammalian cells. The T7 transcripts, which account for as much as 30% of the total cytoplasmic RNA at 24 hr after infection, are largely uncapped. To ***improve*** the translatability of the uncapped RNA, the encephalomyocarditis virus (EMCV) untranslated region (UTR) was inserted between the T7 promoter and the chloramphenicol acetyltransferase (CAT) gene. Experiments with a reticulocyte extract demonstrated that the EMCV UTR conferred ***efficient*** and cap-independent ***translatability*** to CAT RNA synthesized in vitro by T7 RNA polymerase. In cells infected with recombinant vaccinia viruses containing the T7 promoter- ***regulated*** CAT gene, the EMCV UTR ***increased*** the amount of CAT RNA on ***polyribosomes*** . The ***polyribosome*** -derived CAT RNA, which contained the EMCV UTR, was translated in vitro in a cap-independent fashion as well. Use of the EMCV UTR significantly ***enhanced*** the vaccinia/T7 hybrid expression system as it resulted in a 4- to 7-fold ***increase*** in total CAT activity. A further .simeq.2-fold ***improvement*** was achieved by incubating the cells in hypertonic medium, which favors the translation of uncapped picornavirus RNA over cellular mRNAs. With this newly modified expression system, CAT was the predominant protein synthesized by infected cells and within 24 hr accounted for >10% of the total cell protein.

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